



[illegible]

**RESULT**      **2**

JC7531  
calcium transport protein, CatI - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: JC7531  
R:Peng, J.B.; Chen, X.; Berger, U.V.; Wieremowicz, S.; Morton, C.C.; Vassilev, P.M.; Brownlow,  
Biochem. Biophys. Res. Commun. 278, 326-332, 2000  
A>Title: Human calcium transport protein CatI.  
A:Reference number: JC7531; MUID:20551480  
A:Accession: JC7531  
A:Molecule type: mRNA  
A:Residues: 1-725 <PEN>  
A:Cross-references: CB:AF304463  
C:Comment: This protein, a member of a family of Ca<sup>2+</sup> channels, has a role in cellular c  
line and kidney.  
C:Genetics:  
A:Gene: CatI  
A:Map position: 7q33-q34  
C:Keywords: calcium channel; calcium transport; intestine; kidney; transport protein; trn

Query Match	15.88	Score 634	DB 3	Length 725
Best Local Similarity	29.28	Pred. No. 4.1e-41		
Matches 187	Conservative 115	Mismatches 243	Indels 96	Gaps 20

[illegible]

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Db 331 MGLAIIYLLIICIFMCCIRYLRKTRTNNRSPRNTLLQOKLLQEAVMFKDKDIRLVEL 390
QY 438 LILGGIYLLVGOIYMYRRHY--FWISTIDYFELLFLFOALLTVVSOYLCFLAIEMT 495
Db 391 VTVIGAIILILEVPDIFRFMVGTRFFGOTILGCFHVLITTYAFMVLNVMILISASGE 450
QY 496 LPLVASALVGLMLLKYTRGFORTGISYVMIOVLIRDLRFLLIYLVLEFGFAVALVS 555
Db 451 VYPSFALVGLCMVMYFARGFOLGFTIILQKIMFGDLMRCMLAVVILGFASAFYI 510
QY 556 LSGEAMRFEALPTGNATESVQPMFGQDEBNGAOYKQILEASLELKFYTGMELAFOED 615
Db 511 IFQ-----TEDPELCHFYDYPMALSTEEFL-LTIIDSPANYND 550
QY 616 LHRFGVLLLLAYLLVLLTYILLMLLMLLSEFYVNSATDSWSIMKLQKASVLENGY 675
Db 551 LPF--MYSYIAAPAIATITLLMLNTLLIAMGDTHMRYAHERDELMRAQIATVIMLERKL 608
QY 676 ---WY-----CRKQKRGVMILVTYTKDGSDDEWKCRAVEE 708
Db 609 PRCLMPRSGIGREGIGL-----DHWELFRVED 635

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RESULT 3  
T33026  
hypotheoretical protein T09A12.3 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T33026  
R:Hawkins, J.; Fulton, B.; Gillam, B.  
submitted to the EMBL Data Library, February 1998  
A:Description: The sequence of *C. elegans* cosmid T09A12.  
A:Reference number: Z21265  
A:Accession: T33026  
A:Status: preliminary: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-900 <HAM>  
A:Cross-references: EMBL:AF047660; PDB:1AC04431.1; GSPDB:GN00022; CESP:T09A12.3  
A:Experimental source: strain Bristol N2; clone T09A12  
C:Genetics:  
A:Gene: CESP:T09A12.3  
A:Map position: 4  
A:Intons: 437/; 867/; 2607/; 3967/; 4242/; 4951/; 5177/; 5533/; 6913/; 7413/; 7807/;

Query Match	10.3%	Score 414	DB 2	Length 900
Best Local Similarity	24.2%	Pred. No. 6.7e-24		
Matches 183	Conservative 113	Mismatches 253	Indels 206	Gaps 32

QY	61	RKGASQPPDRPRERDROLFNANSGVPEDLAGLPEYLSKTSKYL-----	1DSEYTE	112
Db	98	KKKGKS---GPPVLD---FNOEGENVGD-----LKKALKLIDGGKGRNKSRE		144
QY	113	-----GSGKTCMKAVLNLRKGVNACILPLRLQIDRDSGNPOPLYNAACTIDDYRGH		164
Db	145	ISMKLEEGSGMGETITIGCCILHASDINHAKYLIDY-----YKRLNDIHSDFY-GL		198
QY	165	SALHAIIEKRSLOCYKLLLVENGANVHARACGRFF-----QKSGGT-----		204
Db	199	SPLHAIITINDOCKLVYKRLKLGADVNSKCYGAFCADQKKSRTDSLEHEVELSLKTNV		258
QY	205	---CFYGGELPLSLAACTKQMDVSYLLENPHQAPASLQATDSOGNTVLHALVMISDNSAEN		262
Db	259	TGNMYLGSEYPLSPACALNQPSFRLLAFAKNP---NQDITNGNSVYHMCYI-----HEN		310
QY	263	IATVTSMTDGLLQAGARLCPTVYQLEDIRLQDITPLPKIAAKEGKIETFRHLQREFSGLS		322
Db	311	MA---MEKLLAECGASL-RTV-----NKOSLSPLTIAAKLAKKEMDEILLEEGDSV-		358
QY	323	HLSKRTFMWCQGPRAVSLYLDASVDSCEEN-----SVLEETIAFHCKSPRHRYVLEP		375
Db	359	-----WAAGDASSTVYPLAKIDITINETGELNENASLSLVVYGGQTVHELLELDG--		408

[illegible]

RESULT 4  
 T20312  
 hypothetical protein F28H7.10 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 15-Oct-1999 #sequence-revision 15-Oct-1999 #text-change 29-Oct-1999  
 C:Accession: T20312; T21533  
 R:Matthews, P.  
 submitted to the EMBL Data Library, June 1996  
 A:Reference number: Z19255  
 A:Accession: T20312  
 A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-790 <WIL>  
 A:Cross-references: EMBL:Z74030; PIDN:CAA98449.1; GSPDB:GN00023; CESP:F28H7.10  
 A:Experimental source: clone D1054  
 R:Berts, M.  
 submitted to the EMBL Data Library, May 1996  
 A:Reference number: Z19435  
 A:Accession: T21533  
 A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-790 <WIL>  
 A:Cross-references: EMBL:Z72508; PIDN:CAA96644.1; GSPDB:GN00023; CESP:F28H7.10  
 A:Experimental source: clone F28H7  
 C:Genetics:  
 A:Gene: CESP:F28H7.10  
 A:Map position: 5  
 A:Intons: 46/2; 89/3; 129/1; 157/1; 201/1; 264/2; 349/3; 406/3; 487/3; 543/2; 580/1; 67

```

Query Match          9.88 : Score 392.5 : DB 2 : Length 790 :
Best Local Similarity 25.38 : Pred. No. 2.6e-22 :
Matches 182 : Conservative 106 : Mismatches 243 : Indels 189 : Gaps 35

OY      61  RKGTGASOPD--PNRDRDRLFNAVSRGVPEDLAGLPEYLKSKTSKYL-----TDSEYT 111
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      101  KKGKGGKSGSPNLLDFEDDQO-----AEMAG--DLKALKLKLLDGGKGGKSGSEKYR 147
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      112  E-----GSTGKTR-----CLMK--AVLTAKLDGVAACLTPLQLIDRDSGNPQ--LYNMAC 156
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      148  EMMVSVDERGSMGEULLAICLLQSGSALNNL-----IARRLINFPKLLINDIC 194
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      157  TDDYVRGHSALHIAIEKRSLLQCVKLIVGANGVHARACGRF-----QKQGT----- 204
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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D	b	195	VSEEYTGSLPHLAIYNQDQFISLLRLGADLNQCYGAFFCADDQKASRFDLSLEHEV	254
Q	y	205	-----CFFGELPLSLACTKQMDVSYLLENPHQSPASLQATDSQNTVLHALVM	254
D	b	255	ELTKNTVYTGSMYGEYPLSFALICMGHDLFRMLLA---KKAVLSAQDTNGNTALH-LCV	310
Q	y	255	ISDMSAENIALVYSMTYDGLLQAGARLCPTVQLEDINLDLPLPKAAK-EKGIELFRHI	313
D	b	311	IHDR-----MDMLPAVLEAGNII-----RLANKONLTALTAAKLAKTESIOHL	355
Q	y	314	LQREFSGLSH--LSRKPTFW-CYGPARYSLYDLASDSEENSYLEITIAFHC-----	362
D	b	356	--ELMDLDIEOILDEK---WKAYG-----RALMRLSLGEIFFEYCCPCVAYML	398
Q	y	363	-----KSPHRHRMV-----LEPLNKLQAKWDLIPKFFLNCULIYMFETFAVAHQ	412
D	b	399	RPSATTEHLTRGAINDDGETSTNSTNYLQWMA-----IDIOGLIAM---YSAMPYH	449
Q	y	413	PTLKQAPHLKAEVNSMLTGHILILLAGIYLLVGOLMYTFMRHRHFWISFIDSYEDI	472
D	b	450	GWFR-----LGCIMTIIYMLFOILDFGDRIIRIFQKWF-----NFLAKPAK	493
Q	y	473	LFLRQALLTVSSQVLCFLAI---EWYL-----PLVSAVLGLGNILNLYTRGQNHGIYSV	525
D	b	494	LMKGAFLFIITISPCRLACSPHEPFEPLTDNTMAIISILLYQHFLYKRAIPFVGPVLL	553
Q	y	526	MIQVILIRDLRFLRLIYLVLPFGFAVALVLSQEWARPARPAGPNATSEVQDEGOEDBG	585
D	b	554	MYVTIITFDLVRFAMYSISLFGSOSFYLIPTSCERDS-----YAIKKIDPM-----	601
Q	y	586	NGAOYRGILE---ASLELFTKTIQMGELAFQF-----OLHFRGVYLLLLAYVLLTYIL	636
D	b	602	-GSEFNMINMENPDALLRTFIMTIGFEFSVLYREMSACDNFMKMIKGLTFVIFEFVSIL	660
Q	y	637	LNLNLILMSEYTVNSVATSDMSIMTKLOKASVLEMGNGYMWCKRKQORQAVMLTVGTKPDG	696
D	b	661	QENLLIAMMTTETETFL-TRREKMKQOMQAVILIMLEMGISPASRKMH---LLRYTRPFG	715

RESULT 5  
T37241  
Olfactory channel protein osm-9 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text-change 21-Jul-2000  
C:Accession: T37241  
R:Colbert, H.A.; Smith, T.L.; Bargmann, C.I.  
J. Neurosci. 17, 8259-8269, 1997  
A:Title: OSM-9, A novel protein with structural similarity to channels, is required for  
A:Reference number: Z21639; MUID:97477445  
A:Accession: T37241  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-937 <COL>  
A:Cross-references: EMBL:AF031408; NID:g2642589; PIDN:AA87064.1; PID:g2642590  
C:Genetics:  
A:Gene: osm-9  
A:Map position: IV  
A:Keywords: transmembrane protein

	Query Match	9.1%	Score 364;	DB 2;	Length 937;	
	Best Local Similarity	23.9%	Pred. No. 5.4e-20;			
	Matches 160;	Conservative 101;	Mismatches 254;	Indels 154;	Gaps 23	
QY	LKRTSKYLTDSEYE-----GSTGKTCLMAVNLKDKGNACILPLDIRDSCN	147				
DQ	103 LSEESVDMQGRFKEHYALMKLNKRGVGEN-LIHLRLREQVCYETARLL-LRFRG-	159				
QY	148 PQLPVNAOCTDDYYRGSHALIAIEKRSLOQCVLKLVENGANVAHAAAGRF-----	198				
DQ	160 ---MANDIYLDDEQGCGSALHAIYVHDDEYEPYSLLNSKADVNARAAGCFELPDPFKLTN	216				
QY	199 --QKGQGTCEYFGGLPLSLAACCTQMDDVSYLLENPHOPASIQATDSOGNTVLAHALMIS	256				





QY	213	ISLACTOMDVVSVILEPHOPASIQATQDSGNT-----VLHALMISDMSAENIALVTS	268
Db	109	VAVAEVLLQMEETNN--KEGQPSYMEAVDRKSKFTFYDTFLILAAARNNEIILKI---	162
QY	269	MYDGLLQAGARL-----CPVQLQED-----IRNLQDLTPPLKLAKEG	305
Db	163	-----LLDRGATPLPMHDYKCGCDECVTSQTPTDSLHRSQRIYARALASIALSSNDP	218
QY	306	KIEIFRHLQREFSLSHSKFTWCYGPRAVSLYDLAS--VDSCEANSVLEITAFCK	363
Db	219	VLTAAQ--LSWELKRLQAMESEFRAE-YTEMKQWQDGTSLDHARTSMELVNLNHN	275
QY	364	SP-----HRRMYVLEP--LNKLLQAKWDLIPKF-----	391
Db	276	EPSHIWCIASETLERKLAIRYOKTFVAHPNVQQLAAIWTYGLDGFQEOASQQLMD	335
QY	392	FLNPLCNL-IYWFIFTAVAYHQPITLKKQAAPHLK-AEYGNSSMLTG-----HILIL	441
Db	336	VYKLCGSEPIY-----SLKYILAPDSEGAKEFRNPPLSSSRPPCSYMFMLL	383
QY	442	GGIYLLVQGL-----WYF-----WRRH-----VF-----	460
Db	384	GAASLRVQIYTFPELLAFPMMLTMLEDWRKHERGSLPGPIELAIITYINALIFEELKSY	443
QY	461	-----IW--ISFISYFELLFLF--QALLTVASOVLCPLATEWY-----PL	498
Db	444	DGLFEYIDMLNIIVDIYSIMFYTWILCRATAMVLYVHRDLFRGIDPFPRRHHMPPDP	503
QY	499	IYS-----ALVGLMNLILYYTRGFQHTGIYSVMIQKYLRLDLRFLLIYVFLRFAVA	552
Db	504	ILSEGAFAAGWFSYLIKLVHIFSINPHLGPIQVSLGRMI-DIIKEFFYTLVLEPAFG--	560
QY	553	LVSLSGEAMRRPAPGPRNATESVQPMQEGDEBGNNA-----QYRILASLELFFFTIGM	607
Db	561	-CGLMQLLMY-YAELEKKNCYHLHPDVADFDQERACTIWRFSNLPFTSOSLEFVASFGL	618
QY	608	GELARQEQ-----OLHFRGWLLLLLAIVLLTYILLNMLIALMSFVNSVATDSMCIKIQ	663
Db	619	VDLVSEFDLAGIKSFIRFPALLMFGSYVINIITVLLNMLIAMSNSYQIISERADIEWKFA	678
QY	664	KA 665	
Db	679	RS 680	
RESULT 10			
J00092			
trp protein - fruit fly (Drosophila melanogaster)			
C:Species: Drosophila melanogaster			
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 17-Nov-2000			
C:Accession: J00092			
R:Montell, C.; Rubin, G.M.			
A:Title: Molecular characterization of the Drosophila trp locus: a putative integral mem			
A:Reference number: J00092; MUID:90180449			
A:Accession: J00092			
A:Molecule type: mRNA			
A:Residues: 1-1275 <MON>			
A:Experimental source: Strain Oregon R			
C:Comment: trp protein is expressed predominantly in the rhabdomeric membranes of the ph			
C:Genetics:			
A:Gene: trp			
A:Cross-references: FlyBase:FBgn0003861			
C:Superfamily: TRPC3 protein			
C:Keywords: transmembrane protein			
F:334-354/Domain: transmembrane #status predicted <TM1>			
F:378-401/Domain: transmembrane #status predicted <TM2>			
F:419-436/Domain: transmembrane #status predicted <TM3>			
F:457-471/Domain: transmembrane #status predicted <TM4>			
F:504-527/Domain: transmembrane #status predicted <TM5>			
F:612-630/Domain: transmembrane #status predicted <TM6>			
F:636-661/Domain: transmembrane #status predicted <TM7>			

Query Match	4.8%: Score 190.5; DB 2; Length 1275;
Best Local Similarity	19.9%: Pred. No. 2,4e-06;
Matches 130; Conservative	98; Mismatches 233; Indels 171; Gaps 27;
OY 153	NAOCTDDYYRGHSALHAIIEKRSLOCVKLIVENGANHARAAGRPFOGQCTCFYFGELP 212
DB 62	NINCDPNNR--SALISAISENENEDMNVILLEHNIEV-----GDALLHAISEBY 108
OY 213	LSLACTKOWDVSVSLLENPHOPASLQATDSQGNV---LHALWISDMSNSENTALVTSM 269
DB 109	VEAVELLQWETNH---KEGQPTSMEWAVDSKSTFYVDITPLILAAHRNYELIKI--- 162
OY 270	YDGLLOAGARL-----CPVQLED-----IRNLODTPYLKAAEGK 306
DB 163	---LIDRGATPLPMHDVCGCGDECVTSQTTSDLSRHSGSRINAWALASSTIALSRDPV 219
OY 307	TEIFPHILIQREPSGSLHSKRFTENCYCPRVAVSLYDLAS--VDSCEENSVEIETAFICKS 364
DB 220	LTAFG--LSWELKRLQAMESEFRAE-YTEMQMYODEFSTSLDHARTSMELVLMNFNHE 276
OY 365	P-----HRRHVVLP--LNKLQAKWDLIPKF----- 391
DB 277	PSHDWICGQROGTLERLKLTARIYKOKFTVAHPNVNQQLLAIWYDGLGCFGRKKQASQQLMD 336
OY 392	FLNPLCNLIYWFIFTAVAYHOPTLKKAAPHLKAEVGNMILTGHIILILGCIYLLVQOL 451
DB 337	VKLTCGSPRIYSLKYLIPDSEGAKFMRKPEVKFTITHCSYM--FFMLLGLAASLRYVOI 394
OY 452	-----WYF-----WRRH-----VF-----I 461
DB 395	TFELLAFPMMLTMLEDNRKHERGSLPGIELAIIITYMALIFEEELKSLYSQGLFEYIMDL 454
OY 462	W--ISFIDSYFELLFLF--QALLTVVSOVLCFLAIEWYL-----PLIVS-----A 502
DB 455	WNIVDIYISNMFYVWILLCRATAWYVHRHDLDFRGIDYFPRHHNPPEDPMLLSGGAFAAG 514
OY 503	LVLGLWNLTYTRGQHNGITSVMIQOKITLDDLRLPILITYVLPFGFPAVALYSIOEAMR 562
DB 515	WVFSLKLIVHIFSINPHGLPQVLSIGRNIIT-DIKKEFFITYLVLPFAFG--CGINQLIMY 570
OY 563	PEAPTPNATESVOVPMEGQEDENGCA-----QYRGILEASLELFEKTIQMGELAFQE-- 614
DB 571	YAELEKKCKCHLHPDVAADFPDOEACTIWRPFNSLNETFETSOLESMAFSGLDVLSFDLAG 629
OY 615	QLHRRGVALLLLAYVLLTYIILNMLIAMSTVNSVARDMSIKKLQKA 665
DB 630	IKSFTRWALLMGFSYVINITVILLNMLIAMSNYSOIISRATQEMKFAAS 681

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RESULT 11
138361
TRPC1 protein - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 04-Sep-1998
C:Accession: I38361
R:Wes, P.D.; Chiversich, J.; Jeromin, A.; Roseberry, C.; Stetten, G.; Montell, C.
Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995
A:Title: TRPC1, a human homolog of a Drosophila store-operated channel.
A:Reference number: I38361; MUID:96003837
A:Accession: I38361
A:Status: preliminary; translated from GH/EMBL/DBDB
A:Molecule type: mRNA
A:Residues: 1-810 <RES>
A:Cross-references: EMBL:X89066; NID:g1019786; PID:g1019787
C:Superfamily: TRPC3 protein

Query Match 4.38; Score 174; DB 2; Length 810;
Best Local Similarity 19.18; Pred. NO.2.5e-05;
Matches 139; Conservative 116; Mismatches 244; Indels 228; Gaps 33;

```

Oy 86 GVPEDLADLPEP-----LSKTSKYLDSEYTBESTGCTCMKAV----- 124  
 Db 37 GAPPSPGOLPPSPMAAMAAALPYSTDLSGASSSSSLPSSSSSPNVMAKLDKRVKEENT 96  
 Oy 125 LNLKGDVAC-----LLPLQIDRDGSGNPOLVYNAACCTDDYDYGSHALHATEKSLQ 177  
 Db 97 LNEKFLFLACDQGDVYMKKILE--ENSSGD-----LNICVD--VLGRNAVITTIENEMLD 149  
 Oy 178 CVKLLVENGANYHARACGRFFQKGCTCF--YFGEPLSLAACKQWDVSYLLE----- 230  
 Db 150 ILQLLLDYG-----CQKLMERIQNPESYTFMDVAPVILAAHRNNRYEILTMCLKQDVSL 202  
 Oy 231 -NPH-----QASIQADDSQNTVYLHALVMSD 257  
 Db 203 PKPHAVGCECTLCSAKNNKDSLRSRFRIDYIRCLASPALMLTEE--DPLRAFELSLAD 260  
 Oy 258 -----NSAENIALVTSMYDGLLOAGARCLCPVOLEDIRN----- 291  
 Db 261 LKELSLVEVERNDYEELAROCKMFAKDLLQAR--NSRELEVIINHTSSDEPLDKRLL 318  
 Oy 292 --LQDLPPLKLAKEGKLEIFRHILQREFSGLSHLRSKFTWCYGPVRSLYDLASVDSQ 349  
 Db 319 EERNMLSRLLKLAIKYN-----QKEF-----VSQSNQ 344  
 Oy 350 EENSYLELIIAHCSPRHR-----MYLE-----PLNKL-----QAKDLDLPKFFL 393  
 Db 345 QO--FLNTVFGQMSGYYRRKPKCKIMTVLTVGIEWPVLSLCYLTAAPKSOGRRIITPPEM 402  
 Oy 394 NPLCLNLYMEFT-----AAVYHOPFLKQAAPLKKAEGNSMLTGHIILIGIYLL 447  
 Db 403 KFIHGASYFTFFLLLNLYSLVYNEDK-----KNTMGPALERIDYLLIL-----WI 448  
 Oy 448 VQQLWYEMRRHVFYIWSFIDSYFE-----ILFLQA--LLTVVSGVLCEFLAI-----E 493  
 Db 449 IGMWSDIKR--LMYEGLEDPLEESRNQSLSPVNSLVLAFALKVVAHNKPFHDEADKRD 505  
 Oy 494 W--YPLPLYSALVGLWLLLYTTRGFOHTGIYSW-----IQKYLRLDLRPLLYVFL 546  
 Db 506 WDAFPHPLTVARGLFPAFVAVLSYLRLEFMYTTSSILGPIQISGOWLODFGFLGFWLLVL 565  
 Oy 547 FGEFALVLSLOEARPPAPTPGNATESVOPMEGODEGNCAGQYAGLLESLDLKFTIG 606  
 Db 566 FSTITGLQQLDYDKG-----TSKEQKDCVGIFCEQSSMDT--FHSFGTCFALFWYIFS 617  
 Oy 607 MGELAF-----QEQLFHFGMVLLDLLAVVLLLYLLIYLLIMLMLALMSEFVNSVATDSMS 658  
 Db 618 LAHVAIFFYTRSYGSELQSFYGAV--IYGTYNVVYVLYTLKLVAMLHKSFQLIANHEDK 675  
 Oy 659 TWKLOKA 665  
 Db 676 EWKFARA 682

RESULT 12  
 H71274  
 Probable ankryin - syphilis spirochete  
 C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: H71274  
 R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Dodson, R.; Gwinan, R.;  
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.;  
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
 Science 281, 375-388, 1998  
 A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
 A:Reference number: A71250; MUID:98332770  
 A:Accession: H71274  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-934 <COL>  
 A:Cross-references: GB:AE001254; GB:AE000520; NID:93323148; PIDN:AA65803.1; PID:933231414  
 A:Experimental source: strain Nichols  
 A:Genetics:  
 A:Gene: TP0835

C:Superfamily: syphilis spirochete probable ankyrin; ankyrin repeat homology  
F:281-313/Domain: ankyrin repeat homology <AN2>

Query Match	4.28;	Score 167.5;	DB 1;	Length 934;
Best Local Similarity	27.68;	Pred. No. 9.7e-05;		
Matches	72;	Conservative	37;	Mismatches 95;
			Indels	57;
			Gaps	10

QY	76	RDFFNANVSRCVPDLAGLREPLYSKTSKYLTDSEYTGSGNGKCLMKAVYN-----	126
Db	448	RDPLHVAASRRALHDIY--KFLREPRQOM---IARDTGNTLTHAYVANDDRANGEFL	500
QY	127	LKDGVNAC-----ILPLLDIDRDSGNPOPL-----VNAQCTDDYVGRGSHALIAIEKR	174
Db	501	MREGADIFSTNVHGVSPKLTALTSSGREDILTAANVHADTG---GNTPLHLACEMK	556
QY	175	SLQCCKLLVENGANVHARACGRFFQKQGGTCFYTGELPLSLAECTKMDVYVSYLLE-NPH	233
Db	557	LTOAINGILRLRGAETLEANNLQO-----ETPLPSAVKSDAEAVISILHLPOAG	603
QY	234	QPSALQATDSOGNTVLAHALVVISDSNAENIALVTSMTDGLLOAGARCLPTVLEDIRNLQ	293
Db	604	NPALVDARDADAGNTVLAHCAYKMSALRSADVL-----IREADAR---HYSLNLRNLS	652
QY	294	DLTPKLAAKEGKLEIFRRHIL	314
Db	653	GKRPDLHLAARAGNVDFIRLL	673

RESULT 13

hypothetical protein M05B5.6 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T23729  
R:Gardner, A.  
submitted to the EMBL Data Library, April 1996  
A:Reference number: Z19790  
A:Accession: T23729  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-481 <WIL>  
A:Cross-references: EMBL:Z171265; PIDN:CAA95836.1; GSPDB:GN00019; CESP:M05B5.6  
C:Experimental source: clone M05B5  
C:Genetics:  
A:Gene: CESP:M05B5.6  
A:Map position: 1  
A:Introns: 50/2; 99/1; 133/3; 185/3; 229/3; 402/3; 457/3

Query Match 3.98; Score 157.5; DB 2; Length 481;

Best Local Similarity 23.08, FREQ. NO. 0.00024;  
Matches 90; Conservative 58; Mismatches 149; Indels 95; Gaps 17;

[illegible]

[illegible]

RESULT 14

ankyrin - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 17-Nov-2000  
C:Accession: T13940  
R:Dubreuil, R.R.; Yu, J.  
Proc. Natl. Acad. Sci. U.S.A. 91, 10285-10289, 1994  
A:Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin in *Drosophila*  
A:Reference number: Z17820; MUID:95024098  
A:Accession: T13940  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1549 <DUB>  
A:Cross-references: EMBL:L35601; NTD:9557083; PID:9557084; PIDN:AAC37208.1  
C:Genetics:  
C:Cross-references: FlyBase:FBgn0011747

Query Match	3.9%	Score 157;	DB 2;	Length 1549;
Best Local Similarly	22.8%	Pred. No. 0.0013;		
Matches 91;	Conservative 61;	Mismatches 134;	Indels 114;	Gaps 17;

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QY 101 TSXVLTSEYEGSTGTCTLCKAVLNLKDVANCIPLQLIDBDSGNPQVPLVNAQCTDXY 160
Db 363 TVDVLTL-ALHVAALCHGVKAKVAKLLELDYKAPNPNARAL----- 397
QY 161 YRGSHALHIALEKRSLOCVKLTVENGANVANBARACGRP-----FOGOGCTCFY---- 208
Db 398 -NGFPLTHIACKKRIKMWELLIKHGANIGATTESGTLPLHVASPFMCJINIVYLQÑHEA 456
QY 209 -----GELPISLAACKOMDVSVTLLENPHOPASLQATDSOGNTVHLALWISDNSA 260
Db 457 SADDLPTIRGETPLHLAARANADRIIRILRS---AKVDIAIVEGQPTPLHVASRLG---- 508
QY 261 ENIALVTSMDYGLIOACARLCPTVQJEDINLDLPLKALIAAREKKEIFEIRHLLQ----- 315
Db 509 -NINIML-----LLOHGAEI-----NAOSNDKYSALHIAAREGQENTIVOLLEGAEN 556
QY 316 -----REFSGLSHLRSKFEWCYGPVAVSVLYUDLASVSCSENSVLEI-IAFHCKSPHRHR 369
Db 557 NAYVRKKGTPL-HLACYYGK-QVWVQIILQÑGASIDFOCKNDVTPHLVATHHNNSIYE 613
QY 370 MVLVEPLNKLLOAKWDLIPKFLFNLCLNIYWFIFTAVAYHOPTL---KKOAPR-HLK 424
Db 614 LLLKNGSSPNLCAR-----NGCAlHIACKKNVLEIAMQLQHGADAVNIISGFSPLHLA 669
QY 425 AEVGN-----SHLL-----TGHIIL 439
Db 670 AOGGNVMDVOLLLEYGVISAARKNGTLPLHVAOQGHVAV 709

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## RESULT 15

142/14  
ankyrin 3, splice form 2 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 04-Mar-2000  
C:Accession: T42714  
R:Peterson, L.L.; John, K.M.; Lu, F.M.; Elchev, E.M.; Higgins, A.; Ylarnas, M.; Turtzo, I.  
J. Cell Biol. 130, 313-330, 1995  
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene  
the repeat domain.  
.:Reference number: Z2237; MUID:95340633

A:Accession: t42714  
A:Status: preliminary; translated from GB/EMBL/DBD  
A:Molecule type: mRNA  
A:Residues: 1-1765 <PEP>  
A:Cross-references: EMBL:LA0633; NID:g710548; PID:g710551; PIDN:AAE01605.1.1  
A:Experimental source: strain C57BL/6J; kidney  
C:Genetics:  
A:Gene: Ank3  
A:Map position: 10  
A:Introns: 1587/1  
C:Superfamily: ankyrin; ankyrin repeat homology  
C:Keywords: alternative splicing

Query Match	3.8%;	Score 151;	DB 2;	Length 1765;
Best Local Similarity	27.7%;	Pred. No. 0.0044;		
Matches	78;	Conservative	43;	Mismatches 91;
			Indels	70;
			Gaps	14;

[illegible]

Search completed: July 18, 2001, 15:59:29  
Job time: 162 sec



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